

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/573,794A
Source: IFNO
Date Processed by STIC: 3/5/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/573,794A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.~~
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please **do not use** "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 03/05/2007

PATENT APPLICATION: US/10/573,794A

TIME: 14:44:41

Input Set : A:\Sequence Listing.txt

Output Set : N:\CRF4\03052007\J573794A.raw

3 <110> APPLICANT: Japan Science and Technology Agency
 5 <120> TITLE OF INVENTION: Royal Jelly Peptide
 7 <130> FILE REFERENCE: 04F039PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/573,794A
 C--> 9 <141> CURRENT FILING DATE: 2006-03-28
 9 <150> PRIOR APPLICATION NUMBER: JP 2003-338665
 10 <151> PRIOR FILING DATE: 2003-09-29
 12 <160> NUMBER OF SEQ ID NOS: 17
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 37
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Primer 1
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (1)..(37)
 27 <223> OTHER INFORMATION: i
 30 <400> SEQUENCE: 1
 W--> 31 aaracnwsna thwsngtnaa rggngarwsn aaygtng
 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 29
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Primer 2
 42 <400> SEQUENCE: 2
 43 cgttggcacc agacacgata gatgaaacc
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 29
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Primer 3
 54 <400> SEQUENCE: 3
 55 tttctgaatt ttattaatta ctttattcg
 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 50
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:
 64 <223> OTHER INFORMATION: Fragment 1

Does Not Conform
 corrected sequence sheet
 (pg. 13) ↩

37

See item #11
 on error
 summary sheet

What is the source of
 genetic material?

Invalid
 Response

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/573,794A

DATE: 03/05/2007

TIME: 14:44:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03052007\J573794A.raw

66 <400> SEQUENCE: 4
67 aaaacctcta tctctgttaa aggcgaatcc aacgttgatg ttgtttccca
70 <210> SEQ ID NO: 5
71 <211> LENGTH: 40
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Fragment 2
78 <400> SEQUENCE: 5
79 gatcaactct ctggtttctt ctatcgtttc tgggtgctaac 40
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 40
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Fragment 3
90 <400> SEQUENCE: 6
91 gtttctgcag tactgctggc tcagactctg gttaacatcc 40
94 <210> SEQ ID NO: 7
95 <211> LENGTH: 38
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Fragment 4
102 <400> SEQUENCE: 7
103 tgcagatcct gatcgacgct aacgttttcg cttaatag 38
106 <210> SEQ ID NO: 8
107 <211> LENGTH: 40
108 <212> TYPE: DNA
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <223> OTHER INFORMATION: Fragment 5
114 <400> SEQUENCE: 8
115 ttttgagat agagacaatt tccgcttagg ttgcaactac 40
118 <210> SEQ ID NO: 9
119 <211> LENGTH: 40
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Fragment 6
126 <400> SEQUENCE: 9
127 aacaaagggt ctagttgaga gaccaaagaa gatagcaaag 40
130 <210> SEQ ID NO: 10
131 <211> LENGTH: 40
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Fragment 7
138 <400> SEQUENCE: 10

What is the source
of genetic
material?

Invalid
Response

Same error

Same error

Same error

Same error

Same error

See item # 11

ON ERROR SUMMARY
Sheet 3/5/2007

RAW SEQUENCE LISTING

DATE: 03/05/2007

PATENT APPLICATION: US/10/573,794A

TIME: 14:44:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03052007\J573794A.raw

139 accacgattg caaagacgtc atgacgaccg agtctgagac 40

142 <210> SEQ ID NO: 11

143 <211> LENGTH: 48

144 <212> TYPE: DNA

145 <213> ORGANISM: Artificial Sequence

147 <220> FEATURE:

148 <223> OTHER INFORMATION: Fragment 8

150 <400> SEQUENCE: 11

151 caattgtagg acgtctagga ctagctgcga ttgcaaaagc gaattatc 48

154 <210> SEQ ID NO: 12

155 <211> LENGTH: 31

156 <212> TYPE: DNA

157 <213> ORGANISM: Artificial Sequence

159 <220> FEATURE:

160 <223> OTHER INFORMATION: LIC Forward

162 <400> SEQUENCE: 12

163 ggtattgagg gtcgcaaaac ctctatctct g 31

166 <210> SEQ ID NO: 13

167 <211> LENGTH: 33

168 <212> TYPE: DNA

169 <213> ORGANISM: Artificial Sequence

171 <220> FEATURE:

172 <223> OTHER INFORMATION: LIC Reverse

174 <400> SEQUENCE: 13

175 agaggagagt tagagcccta ttaagcgaaa acg 33

178 <210> SEQ ID NO: 14

179 <211> LENGTH: 162

180 <212> TYPE: DNA

181 <213> ORGANISM: bee

183 <220> FEATURE:

184 <221> NAME/KEY: misc_feature

185 <222> LOCATION: (1)..(162)

186 <223> OTHER INFORMATION: unknown

189 <220> FEATURE:

190 <221> NAME/KEY: CDS

191 <222> LOCATION: (1)..(162)

192 <223> OTHER INFORMATION:

W--> 194 <400> 14

195 aaa aca tca atc agt gtc aaa ggc gaa tcg aac gtg gat gtc gtt tcc 48

196 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser

197 1 5 10 15

199 caa atc aac agt ttg gtt tca tct atc gtg tct ggt gcc aac gtg tca 96

200 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser

201 20 25 30

W--> 203 gca gta ctc cta gct caa act tta gtt aat atc ctg caa att nnn atc 144

204 Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Xaa Ile

205 35 40 45

207 gac gct aat gtt ttc gct 162

208 Asp Ala Asn Val Phe Ala

Same errors

RAW SEQUENCE LISTING

DATE: 03/05/2007

PATENT APPLICATION: US/10/573,794A

TIME: 14:44:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03052007\J573794A.raw

```

209      50
212 <210> SEQ ID NO: 15
213 <211> LENGTH: 54
214 <212> TYPE: PRT
215 <213> ORGANISM: bee
217 <220> FEATURE:
218 <221> NAME/KEY: misc_feature
219 <222> LOCATION: (47)..(47)
220 <223> OTHER INFORMATION: The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr,
ile,
221      Met, Xaa, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp,
222      Cys, or Phe.
224 <400> SEQUENCE: 15
226 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
227 1      5      10      15
230 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
231      20      25      30
W--> 234 Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Xaa Ile
235      35      40      45
238 Asp Ala Asn Val Phe Ala
239      50
242 <210> SEQ ID NO: 16
243 <211> LENGTH: 162
244 <212> TYPE: DNA
245 <213> ORGANISM: bee
247 <220> FEATURE:
248 <221> NAME/KEY: CDS
249 <222> LOCATION: (1)..(162)
250 <223> OTHER INFORMATION:
W--> 252 <400> 16
253 aaa aca tca atc agt gtc aaa ggc gaa tcg aac gtg gat gtc gtt tcc      48
254 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
255 1      5      10      15
257 caa atc aac agt ttg gtt tca tct atc gtg tct ggt gcc aac gtg tca      96
258 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser
259      20      25      30
261 gca gta ctc cta gct caa act tta gtt aat atc ctg caa att ctt atc      144
262 Ala Val Leu Leu Ala Gln Thr Leu Val Asn Ile Leu Gln Ile Leu Ile
263      35      40      45
265 gac gct aat gtt ttc gct      162
266 Asp Ala Asn Val Phe Ala
267      50
270 <210> SEQ ID NO: 17
271 <211> LENGTH: 54
272 <212> TYPE: PRT
273 <213> ORGANISM: bee
275 <400> SEQUENCE: 17
277 Lys Thr Ser Ile Ser Val Lys Gly Glu Ser Asn Val Asp Val Val Ser
278 1      5      10      15
281 Gln Ile Asn Ser Leu Val Ser Ser Ile Val Ser Gly Ala Asn Val Ser

```

RAW SEQUENCE LISTING

DATE: 03/05/2007

PATENT APPLICATION: US/10/573,794A

TIME: 14:44:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03052007\J573794A.raw

282		20		25		30										
285	Ala	Val	Leu	Leu	Ala	Gln	Thr	Leu	Val	Asn	Ile	Leu	Gln	Ile	Leu	Ile
286		35		40		45										
289	Asp	Ala	Asn	Val	Phe	Ala										
290		50														

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/573,794A

DATE: 03/05/2007
TIME: 14:44:42

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\03052007\J573794A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6,9,15,18,24,30,36

Seq#:14; N Pos. 139,140,141

Seq#:14; Xaa Pos. 47

Seq#:15; Xaa Pos. 47

VERIFICATION SUMMARY

DATE: 03/05/2007

PATENT APPLICATION: US/10/573,794A

TIME: 14:44:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\03052007\J573794A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:31 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0

L:194 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:192

L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:96

M:341 Repeated in SeqNo=14

L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:32

L:252 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:250